

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 23, 2002, 14:37:43 ; Search time 11.97 Seconds

(without alignments)  
604.892 Million cell updates/sec

Title: US-09-811-118-1

Perfect score: 983

Sequence: 1 MVNATVAAAWLTLMAAACAQ.....VRLQITPVLVKLLKREDL 187

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues 105224

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	338	34.4	180	1	GSHP_HUMAN
2	335	34.1	242	1	GSHP_HUMAN
3	328.5	33.5	169	1	GPO_STN3
4	319	32.5	169	1	GSHP_SCHNA
5	318	32.3	167	1	GSHP_CITSI
6	316	32.1	167	1	GSHP_HELAN
7	311	31.6	197	1	GSHP_HUMAN
8	309	31.4	169	1	GSHP_NICCY
9	308	31.3	197	1	GSHP_MOUSE
10	307	31.2	197	1	GSHP_RAT
11	305.5	31.1	157	1	GPO_LACIC
12	305.5	31.1	193	1	BRUE_ECOLI
13	303	30.8	197	1	GSHP_PIG
14	297	30.2	160	1	BSAA_BACSU
15	288	29.3	162	1	GSHP_YEAST
16	283.5	28.8	157	1	BSAA_BACSU
17	279.5	28.4	163	1	GSHP_CAEEL
18	275.5	28.0	177	1	GSHP_NEIMA
19	274	27.9	163	1	GSHP_YEAST
20	260.5	26.5	158	1	GSHP_SCHPO
21	259	26.3	163	1	GSHP_CAEEL
22	256	26.0	201	1	GSHP_HUMAN
23	253	25.7	167	1	GSHP_YEAST
24	245.5	25.0	201	1	GSHP_RAT
25	243.5	24.8	200	1	GSHP_RABIT
26	243.5	24.8	201	1	GSHP_MOUSE
27	242.5	24.7	221	1	GSHP_HUMAN
28	241	24.5	205	1	GSHP_BOVIN
29	240	24.4	226	1	GSHP_RAT
30	236	24.0	221	1	GSHP_MOUSE
31	234.5	23.9	221	1	GSHP_MACRA
32	231	23.5	226	1	GSHP_MOUSE
33	229	23.3	190	1	GSHP_HUMAN

34	228	23.2	226	1	GSHP_BOVIN	P37141	bos taurus
35	228	23.2	226	1	GSHP_HUMAN	P22352	homo sapien
36	223.5	22.7	190	1	GSHP_MOUSE	O91nc0	mus musculus
37	219	22.3	219	1	GSHP_PIG	O18994	sus scrofa
38	215.5	21.9	221	1	GSHP_RAT	O64625	rattus norv
39	210	21.4	222	1	GSHP_PSEWT	O08368	pseudomona
40	209	21.3	221	1	GSHP_RAT	P30710	rattus norv
41	207	21.1	221	1	GSHP_CANFA	O46607	canis famil
42	201	20.4	224	1	GSHP_CAEEL	O95003	caenorhabd
43	198	20.1	223	1	GSHP_BRUMA	P35665	brugia mala
44	196	19.9	223	1	GSHP_WOCBA	P35666	wuchereria
45	193.5	19.7	221	1	GSHP_DIRIM	P52033	dirofilaria

## ALIGNMENTS

RESULT	ID	GSHP_HELAN	STANDARD	PRT	180 AA.
AC	023968				
DT	15-DEC-1998	(Rel. 37, Created)			
DT	15-DEC-1998	(Rel. 37, Last sequence update)			
DE	30-MAY-2000	(Rel. 39, Last annotation update)			
GN	GPXHA-2				
OS	Helianthus annuus (Common sunflower).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Asteridae; euasterids II; Asterales; Asteraceae; Asteroidaceae;				
OC	Heliantheae; Helianthus.				
OX	NCBI_Taxid=4232;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Drevet J.R., Gagne G., Tourvieille de Labrouhe D., Nicolas P.,				
RA	Dufaire J.P., Ledoligt G., Roedel-Drevet P.;				
RL	Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.				
CC	-1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE				
CC	PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.				
CC	-1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) - oxidized				
CC	glutathione + 2 H(2)O.				
CC	-1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.				
CC	-----				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL; Y14707; CAA75009.1; -				
DR	HSP; P00435; GPR1.				
DR	InterPro; IPR000889; Glut_peroxidase.				
DR	Pfam; PF00255; GSHPx; 1.				
DR	PRINTS; PR01011; GLUTPROXIDASE.				
DR	PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.				
DR	PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.				
KW	Oxidoreductase; Peroxidase.				
FT	ACT_SITE 54				
FT	SEQUENCE 180 AA; 20174 MW; E33090EAD2A2ADE0 CRC64;				

Query Match 34.4%; Score 338; DB 1; Length 180;  
Best Local Similarity 43.9%; Pred. No. 9.9e-26;  
Matches 69; Conservative 26; Mismatches 54; Indels 8; Gaps 2;

OY	28	FAVNRIGKLVISLEKRGVSLVNVNASEGFTDQHYRALQDLDGPHFNVLAFCN 87	
DB	25	FSDKDKGQDVELSKKKGVLLIVNVAQCFTNSYPELTLLYXKKQCGFEIIAFCN 84	
OY	88	QFGQGPDSNKEIESFACFTYSVSPMFESKIAVTGTGAHPAFKYLAQTS---GKEPTWN 143	

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Db      85 QFGQEPGSGNEIOWFACTRFKAEPYFVFSKVVNNGKEADPLYKFLKSGFGLGDSIKWN 144
QY      144 FMKYLVAIPDGKVVGAMPDPTVSVEVRLOITVALVRKLI 180
Db      145 FTKFLVDREGKVVDRAPPTTS-----PLSTIEKDITKLL 177

RESULT  2
GSHY_ARATH STANDARD: PRT: 242 AA.
AC      P52032.
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Glutathione peroxidase homolog, chloroplast precursor (EC 1.11.1.9).
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RA      Gachotte D., Benveniste P.;
RT      "Cloning and sequencing of a glutathione peroxidase homologue from
RT      Arabidopsis thaliana."
RL      (In) Plant Gene Register PGR95-133.
CC      -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) -> oxidized
CC      glutathione + 2 H(2)O.
CC      -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X89866; CAAG1965.1; -.
DR      HSSP: P00435; IGPI.
DR      InterPro: IPR000889; Glut_peroxidase.
DR      Pfam: PF00255; GSHPX.1.
DR      PRINTS: PR01011; GLUTPROXOXASE.
DR      PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR      PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW      Peroxidase; Oxidoreductase; Transil peptide; Chloroplast.
FT      TRANSIT 1 64 CHLOROPLAST (POTENTIAL).
FT      CHAIN 65 242 GLUTATHIONE PEROXIDASE HOMOLOG.
FT      ACT_SITE 111 111 BY SIMILARITY.
SQ      SEQUENCE 242 AA; 26814 MW; 3A7031CCB416B57 CRC64;

Query Match 34.1%; Score 335; DB 1; Length 242;
Best Local Similarity 41.2%; Pred. No. 2.7e-25;
Matches 70; Conservative 24; Mismatches 66; Indels 10; Gaps 2;

QY      17 ACAQODEYDFKAVNIRKLVSLKRYGVSLLVNVNASECGFTDQHYRALQDLORDLGP 76
Db      71 ARAAAKTYHDFTYKIDKDALNFKGVMLIVNVAASGGLTSSNSLSLYEKYK 130
QY      77 HHENVLAPPCNOFGQEPDSNKEIESFACRTYSVSFPMFSKIAVGTGAHPAFKYLAQTS 136
Db      131 OGFEILAPPCNOFGQEPDSNKEIKQFACRFKAEPFIDKVDVNGSPAPYIEFLKSNA 190
QY      137 G-----KEPTWFMKYLVAIPDGKVVGAMPDPTVSVEVRLOITVALVRKLI 179
Db      191 GGLGLGLIK--WNFEKFLIDKKGVKVERPPTSPFQIEKDIQKLLAEL 237

RESULT  3
GPO_SYNY3 STANDARD: PRT: 169 AA.
ID      GPO_SYNY3

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AC      P74250;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Putative glutathione peroxidase (EC 1.11.1.9).
GN      SLR1171.
OS      Synechocystis sp. (strain PCC 6803).
OC      Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX      NCBI_TaxID=1148;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97061201; PubMed=8905231;
RA      Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA      Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA      Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA      Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA      Tabata S.;
RT      "Sequence analysis of the genome of the unicellular cyanobacterium
RT      Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT      entire genome and assignment of potential protein-coding regions."
RL      DNA Res. 3:109-136(1996).
CC      -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) -> oxidized
CC      glutathione + 2 H(2)O.
CC      -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----
DR      EMBL: D90913; BAA18344.1; -.
DR      HSSP: P00435; IGPI.
DR      InterPro: IPR000889; Glut_peroxidase.
DR      Pfam: PF00255; GSHPX.1.
DR      PRINTS: PR01011; GLUTPROXOXASE.
DR      PROSITE: PS00460; GLUTATHIONE_PEROXID_1; 1.
DR      PROSITE: PS00763; GLUTATHIONE_PEROXID_2; 1.
KW      Peroxidase; Oxidoreductase; Complete proteome.
FT      ACT_SITE 41 41 BY SIMILARITY.
SQ      SEQUENCE 169 AA; 18452 MW; 0DC382089CE39E2 CRC64;

Query Match 33.5%; Score 329.5; DB 1; Length 169;
Best Local Similarity 41.7%; Pred. No. 6.1e-25;
Matches 70; Conservative 20; Mismatches 67; Indels 11; Gaps 2;

QY      19 AQQODEYDFKAVNIRKLVSLKRYGVSLLVNVNASECGFTDQHYRALQDLORDLGP 78
Db      3 AQANNIYGFSSANALDGSFVALRDFEGKVLIIYNVTSQCGFTPO-YQGLQALTNRFGRD 61
QY      79 FNVLAAPPCNOFGQEPDSNKEIESFACRTYSVSFPMFSKIAVGTGAHPAFKYLAQTS 136
Db      62 FTVLGFPCNOFGQEPDSNKEIKFCETRGVFPFLFEVNGVPAHPFKFLTAASPG 121
QY      137 -----GKEPTWFMKYLVAIPDGKVVGAMPDPTVSVEVRLOITVALVRKLI 176
Db      122 MATPLGAGNEDIKWNFTFLVDROGKVVKRYGSIAPDEIADIETKLL 169

RESULT  4
GSHC_SCHMA STANDARD: PRT: 169 AA.
ID      GSHC_SCHMA
DT      01-DEC-1992 (Rel. 24, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Glutathione peroxidase (EC 1.11.1.9) (GPX).
GN      GPX1.
OS      Schistosoma mansoni (Blood fluke).
OC      Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;

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OC Rhadithophora; Eulactophora; Revertospermatia; Mediofusata;  
 OC Neodermatia; Trematoda; Digenea; Strigeida; Schistosomatoidea;  
 OC Schistosomatidae; Schistosoma.  
 OX NCBI\_TaxID=6183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Puerto Rican;  
 RX MEDLINE=92326859; PubMed=1625700;  
 RA Williams D.L., Pierce R.J., Capron A.;  
 RT "Molecular cloning and sequencing of glutathione peroxidase from  
 Schistosoma mansoni";  
 RL Mol. Biochem. Parasitol. 52:127-130(1992).  
 RN [2]  
 RP REVISION TO 43.  
 RA Williams D.L., Pierce R.J., Capron A.;  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBD databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NMRI;  
 RX MEDLINE=95203415; PubMed=7895842;  
 RA Mel H., Loverde P.T.;  
 RT "Schistosoma mansoni: cloning the gene encoding glutathione  
 peroxidase";  
 RL Exp. Parasitol. 80:319-322(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PUERTO RICAN;  
 RX MEDLINE=94171027; PubMed=8125294;  
 RA Roche C., Williams D.L., Khalife J., Lepreste T., Capron A.,  
 Pierce R.D.;  
 RT "Cloning and characterization of the gene encoding Schistosoma  
 mansoni glutathione peroxidase";  
 RL Gene 138:149-152(1994).  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 glutathione + 2 H(2)O.  
 CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS  
 ENCODED BY THE OPAL CODON, UGA.  
 CC -1- INDUCTION: GPX ACTIVITY INCREASES SIGNIFICANTLY AS WORMS MATURE IN  
 THEIR HOST AND IS POSITIVELY CORRELATED TO THE RESISTANCE TO  
 ANTIOXIDANTS.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M86510; AAA29885.2; ALT. SEQ.  
 DR EMBL: L37762; AAC14468.2; ALT. SEQ.  
 DR EMBL: L14329; AAB08485.2; ALT. SEQ.  
 DR EMBL: L14328; AAB08485.2; JOINED.  
 DR HSP: P00435; IGPI.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHPX.1.  
 DR PRINTS: PR01011; GLUTPROXADSE.  
 DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Oxidoreductase; Peroxidase; Selenium; Selenocysteine.  
 FT SE\_CYS 43 43  
 SO SEQUENCE 169 AA; 19424 MW; 55D87788BF9FC10 CRC64;

Query Match 32.5%; Score 319; DB 1; Length 169;  
 Best Local Similarity 43.9%; Pred. No. 6.3e-24;  
 Matches 69; Conservative 21; Mismatches 63; Indels 4; Gaps 1;

OY 26 YDFKAVNIRGKLVSLKRGYSVSLVNVNASECGFTDQHRALDQORDLGPFFHFNWLP 85  
 DB 12 YETVADINGVDVSLERKRGHCVLLIVNACKGCATDKRNYRLOEDMTRLVGKGLRILAP 71

OY 86 CNOFGOEPPDSNKEIESFACRTYSVFFPMFSKIAVGTGAHPAFKYLQO----TSGKEPT 141  
 DB 72 CNOFGOEPPMAEIKFTYERKGVQFDMFSKIKVNSDADDLKRLKSNQHTLNNIK 131  
 OY 142 WNFMYKLVADGKVGAMDPVSVVEEVRILQITALVKK 178  
 DB 132 WNFSEKFLVDROGQPVKRYSPPTAPYDIEGIMWELKK 168  
 RESULT 5  
 GSH2\_CITSI STANDARD; PRT; 167 AA.  
 AC 006652;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Glutathione peroxidase homolog (Ec 1.11.1.9) (Salt-associated  
 protein).  
 GN CSA.  
 OS Citrus sinensis (Sweet orange).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eurosid II; Sapindales; Rutaceae; Citrus.  
 OX NCBI\_TaxID=2711;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=93222490; PubMed=8467085;  
 RA Holland D., Ben-Hayyim G., Falcin Z., Camoin L., Strosberg A.D.,  
 Esbat Y.;  
 RT "Molecular characterization of salt-stress-associated protein in  
 Citrus: protein and cDNA sequence homology to mammalian glutathione  
 peroxidases";  
 RL Plant Mol. Biol. 21:923-927(1993).  
 CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE  
 PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.  
 CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 glutathione + 2 H(2)O.  
 CC -1- INDUCTION: BY SALT STRESS.  
 CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.  
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 CC -----  
 DR EMBL: X66377; CAA47018.1; -  
 DR HSP: P00435; IGPI.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHPX.1.  
 DR PRINTS: PR01011; GLUTPROXADSE.  
 DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
 DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Oxidoreductase; Peroxidase.  
 FT ACT\_SITE 41 41  
 SO SEQUENCE 167 AA; 18596 MW; DB6BDDC363F3260 CRC64;

Query Match 32.3%; Score 318; DB 1; Length 167;  
 Best Local Similarity 39.2%; Pred. No. 7.8e-24;  
 Matches 65; Conservative 28; Mismatches 65; Indels 8; Gaps 2;

OY 19 AQOEDFYDFKAVNIRGKLVSLKRGYSVSLVNVNASECGFTDQHRALDQORDLGP 78  
 DB 3 SQKTSVHDFTVDKADGQVDLSITKGLLLIVNVSQGLFNSNTELSQLYDKVKNKG 62  
 OY 79 FNVLAFFCNOFGOEPPDSNKEIESFACRTYSVFFPMFSKIAVGTGAHPAFKYLQTS-- 136  
 DB 63 LELIAFCNOFGOEPPDSNKEIESFACRTYKFAEPFLFDKDVAGDAAAPLYKHLKSSKG 122  
 OY 137 --GKEPTWNFMYKLVADGKVGAMDPVSVVEEVRILQITALVKKLI 180

Db 123 LFGDSIKMNSKFLVDKGNVVERIAPTTS-----PLSIKDIKRL 164

## RESULT 6

ID GSHZ\_HUMAN STANDARD: PRT; 167 AA.

AC 023970;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Glutathione peroxidase 1 (EC 1.11.1.9).

GN GPXHA-1.

OS Helianthus annuus (Common sunflower).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;

OC Heliantheae; Helianthus.

OX NCBI\_TaxID=4232;

RN [1]

RP SEQUENCE FROM N.A.

RA Drevet J.R., Gagne G., Tourvieille de Labrouhe D., Nicolas P.,

RA Dufauré J.P., Ledolgt G., Roedel-Drevet P.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE

CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized

CC glutathione + 2 H(2)O.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

CC

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DR EMBL; Y14429; CAA74775.1; -.

DR HSSP; P00435; IGPI.

DR InterPro: IPR000889; Glut\_peroxidase.

DR Pfam; PF00255; GSHPX; 1.

DR PRINTS; PR01011; GLUTPROXIDASE.

DR PROSITE; PS00460; GLUTATHIONE\_PEROXID\_1; 1.

DR PROSITE; PS00763; GLUTATHIONE\_PEROXID\_2; 1.

DR Oxidoreductase; Peroxidase.

KW ACT\_SITE 41

FT ACT\_SITE 41

SQ SEQUENCE 167 AA; 18842 MW; CFSAC7ACCT6558C9 CRC64;

Query Match 32.1%; Score 316; DB 1; Length 167;

Best Local Similarity 41.0%; Pred. No. 1.2e-23;

Matches 66; Conservative 23; Mismatches 68; Indels 4; Gaps 1;

OY 20 QOEDQFYDEKAVINRKLVSLEKRGVSLLVNVASECGFTDQHYRALQOLRLDLPHPH 79

DB 4 QSKRTITLDTVDAGKNDVLDLVYKGVLLVNVASKGCLTNSYDELNDQILYKKEKGF 63

OY 80 NVLAIFPCNFGQOEDPSNKEIESFACRTYSVSPMRSKLAVTGTAHPFKYLAQ-----T 135

DB 64 ELIAFPNCNFGQOEDPTGNEIYDFVCTKFSPEPIDKDVNENAPAEFLKTFPGYGI 123

OY 136 SCKEPTFMFKYLVAPDGVKVGAMDPTVSVVEEYRLQITALV 176

DB 124 LGDDIOMNFSKFLVDKNGQVDCYPTTSPLYVERDIQKLL 164

RESULT 7

GSHZ\_HUMAN STANDARD: PRT; 197 AA.

ID GSHZ\_HUMAN STANDARD: PRT; 197 AA.

AC P36369; 043381.

DT 01-JUN-1994 (Rel. 29, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial

DE precursor (EC 1.11.1.9) (GPX4).

GN GPX4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;

RX MEDLINE=94314239; PubMed=8039723;

RA Esworthy R.S., Doan K., Doroshov J.H., Chu F.-F.;

RT "Cloning and sequencing of the cDNA encoding a human testis

RT phospholipid hydroperoxide glutathione peroxidase.";

RL Gene 144:317-318(1994).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98381025; PubMed=9705830;

RA Keiner M.J., Montoya M.A.;

RT "Structural organization of the human selenium-dependent phospholipid

RT hydroperoxide glutathione peroxidase gene (GPX4): chromosomal

RT localization to 19p13.3.";

RL Biochem. Biophys. Res. Commun. 249:53-55(1998).

RN [3]

RP SEQUENCE FROM N.A.

RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.M.,

RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,

RA Phan H., Velasco N., Ganes J., Dangnan L., Poundstone P.,

RA Christensen M., Georgescu A., Avila J., Liu S., Altis C., Andreise T.,

RA Trankelm M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,

RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,

RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,

RA Carraro A.V.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE

CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized

CC glutathione + 2 H(2)O.

CC -1- COPACITOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS

CC ENCODED BY THE OPAL CODON, UGA.

CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.

CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS

CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.

CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

CC

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----

DR EMBL; X71973; CAA50793.1; ALT\_SEQ.

DR EMBL; AF060972; AAC32261.1; ALT\_SEQ.

DR EMBL; AC004151; AAC03239.1; ALT\_SEQ.

DR HSSP; P00435; IGPI.

DR MIM; 138322; -.

DR InterPro: IPR000889; Glut\_peroxidase.

DR Pfam; PF00255; GSHPX; 1.

DR PRINTS; PR01011; GLUTPROXIDASE.

DR PROSITE; PS00460; GLUTATHIONE\_PEROXID\_1; 1.

DR PROSITE; PS00763; GLUTATHIONE\_PEROXID\_2; 1.

DR Oxidoreductase; Peroxidase; Selenium; Selenocysteine;

KW Mitochondrion; Transit peptide; Alternative initiation.

KW MITOCHONDRION (POTENTIAL).

FT TRANSIT 1

FT CHAIN 2

FT CHAIN 197

FT CHAIN 28

FT CHAIN 197

FT INIT\_MET 28

FT INIT\_MET 28

FOR CYTOPLASMIC ISOFORM.

FT SE.CYS 73 73  
SQ SEQUENCE 197 AA; 22128 MW; 1AE3A2DAEC8FCB1 CRC64;

Query Match 31.6%; Score 311; DB 1; Length 197;  
Best Local Similarity 43.9%; Pred. No. 4.5e-23;  
Matches 68; Conservative 25; Mismatches 50; Indels 12; Gaps 4;

OY 18 CAQOE-----ODEYDEKAVNIRGKLVLEKRGSVSLVYVNASGEGFTPOHRAIQLOLR 72  
DB 29 CASRDMRCARSMHESADIDGHNVDKIRGFCVITVNASQCGKTEVNTIQVDLHA 88  
OY 73 DLGPHFNVLAPPCNFGQOEPDSNKEISFACRTYSVSFPMFSKTAIVGTGAPAFKYL 132  
DB 89 RAEGLRLAPPCNFGQOEPDSNKEISFACRTYSVSFPMFSKTAIVGTGAPAFKYL 147  
OY 133 -AQTSGK-----EPTWNEFKYLVADPKVYGAMP 161  
DB 148 KIOPKGGILGNAIKWNFTKFLDKNGCYVRRYGP 182

## RESULT 8

GSHP\_NICSY STANDARD; PRT; 169 AA.

AC P30708;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Glutathione peroxidase homolog 6P229 (EC 1.11.1.9).  
OS Nicotiana sylvestris (Wood tobacco).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; eusteridae I; Solanales; Solanaceae; Nicotiana.  
OX NCBI\_TaxID=4096;  
RN [1]

RP SEQUENCE FROM N.A.  
RC TISSUE=Protoplast;  
RA MEDLINE=92163033; PubMed=1536938;  
RA Criqui M.C., Jamet E., Parmentier Y., Marbach J., Durr A., Fleck J.;  
RT "Isolation and characterization of a plant cDNA showing homology to  
RT animal glutathione peroxidases.";  
RL Plant Mol. Biol. 18:623-627(1992).

CC -1- FUNCTION: MAY CONSTITUTE A GLUTATHIONE PEROXIDASE-LIKE  
CC PROTECTIVE SYSTEM AGAINST OXIDATIVE STRESSES.

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
CC glutathione + 2 H(2)O.

CC -1- TISSUE SPECIFICITY: GERMINATING SEED, APEX, FLOWER, AS WELL AS IN  
CC STRESSED TISSUES.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: X60219; CAA42780.1; -  
DR PIR: S20501; S20501.  
DR HSSP: P00435; IGPI.  
DR InterPro: IPR000889; Glut\_peroxidase.  
DR Pfam: PF00255; GSHPX; 1.  
DR PRINTS: PRO1011; GLUTPROXDAE.  
DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
KW Oxidoreductase; Peroxidase.  
FT ACT\_SITE 43 BY SIMILARITY.  
FT SEQUENCE 169 AA; 18767 MW; 401919069E1E97C7 CRC64;

Query Match 31.4%; Score 309; DB 1; Length 169;  
Best Local Similarity 36.4%; Pred. No. 5.9e-23;

Matches 60; Conservative 31; Mismatches 70; Indels 4; Gaps 1;

OY 16 AACAOEOPDYEFKAVNIRGKLVLEKRGSVSLVYVNASGEGFTPOHRAIQLOLRD 75  
DB 2 ASQSSKPSQSYDPTVVDAGNDVLSYRGKVLIVYVNASQCGLTNSNTDITETIKKK 61  
OY 76 PHEFNVLAPPCNFGQOEPDSNKEISFACRTYSVSFPMFSKTAIVGTGAPAFKYL 135  
DB 62 DQLELTLAPPCNFGQOEPDSNKEISFACRTYSVSFPMFSKTAIVGTGAPAFKYL 121  
OY 136 S-----GKEPTWNEFKYLVADPKVYGAMPYVSVEEVLQITLV 176  
DB 122 KGGFEDSIKWNFSKFLVDKGNVVDYRSPYTPASMERDICKLL 166

## RESULT 9

GSHP\_MOUSE STANDARD; PRT; 197 AA.

AC 070325;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Phospholipid hydroperoxide glutathione peroxidase, mitochondrial  
DE precursor (EC 1.11.1.9) (PBGpx) (GPX-4).  
GN GPX4.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=FAH/B; AND C57BL/6J; TISSUE=Testis, and Myocardium;  
RX MEDLINE=99272820; PubMed=10341094;  
RA Knopp E.A., Arndt T.L., Eng K.L., Caldwell M., Lebeuf R.C.,  
RA Deeb S.S., O'Brien K.D.;  
RT "Murine phospholipid hydroperoxide glutathione peroxidase: cDNA  
RT sequence, tissue expression, and mapping.";  
RL Mamm. Genome 10:601-605(1999).

CC -1- FUNCTION: COULD PLAY A MAJOR ROLE IN PROTECTING MAMMALS FROM THE  
CC TOXICITY OF INGESTED LIPID HYDROPEROXIDES.

CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
CC glutathione + 2 H(2)O.

CC -1- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS  
CC ENCODED BY THE OPAL CODON, UGA.

CC -1- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.

CC -1- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORMS  
CC BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.

CC -1- TISSUE SPECIFICITY: PRESENT PRIMARILY IN TESTIS.

CC -1- SIMILARITY: BELONGS TO THE GLUTATHIONE PEROXIDASE FAMILY.

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

DR EMBL: AF045768; AAC18832.1; ALT\_INIT.  
DR EMBL: AF045769; AAC18833.1; ALT\_INIT.  
DR EMBL: AF044056; AAC14560.1; -  
DR HSSP: P00435; IGPI.  
DR MGD: MGI:104767; GPX4.  
DR InterPro: IPR000889; Glut\_peroxidase.  
DR Pfam: PF00255; GSHPX; 1.  
DR PRINTS: PRO1011; GLUTPROXDAE.  
DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; 1.  
DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
KW Oxidoreductase; Peroxidase; Selenium; Selenocysteine;  
KW Mitochondrion; Transit peptide; Alternative initiation.  
FT TRANSIT 1  
FT CHAIN ? 197 MITOCHONDRION (POTENTIAL).  
FT PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE  
FT PEROXIDASE, MITOCHONDRIAL ISOFORM.













Mon Aug 26 08:01:41 2002

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